PAUL SCHERRER INSTITUT

8th December 2015

The Laboratory of Biomolecular Research at the PSI offers a

Master Project in Macromolecular Crystallography

Diffraction data from crystals play an important role to investigate molecules and complexes at atomic detail. Diffraction experiments are carried out with X–rays, neutrons, or electrons. The technology of X–ray diffraction is advanced and established. Both neutron and electron diffraction are currently moving into the focus of research: the Paul Scherrer Institute is building the first dedicated electron diffraction instrument, and world wide neutron sources are constructed and upgraded.
New diffraction facilities require proper calibration in order to understand the measured data correctly. Crystalline bovine Insulin is ideal to calibrate diffraction instruments [1, 2]. A standard protocol to grow its cubic crystal form routinely produces crystals with about 0.2 mm edge length. Neutron diffraction requires an edge length of at least 1 mm.

Project Goals

The candidate for this project will use micro seeding, macro seeding and dialysis in order to produce crystals of bovine insulin with a volume greater than 1 mm^3. He will find a suitable freezing procedure that maintains the crystal quality. The crystal quality will be assessed by X–ray diffraction at the Swiss Light Source (SLS). Data from neutron diffraction will be collected at Institute Laue Langevin (ILL) in Grenoble or the Forschungsreaktor München FRM-II. He will process the diffraction data and refine the structure against X–ray and against neutron data [3].

Your Skills

The candidate should be experienced with biochemical or chemical laboratory work and should have a basic education in crystallography.
The position includes a monthly allowance and travel expenses will be paid for.

Contact

For further information please contact

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References

[1] I. Dix et al. ‘The EU BIOXHIT standard test crystal’. In: *Acta Crystallogr* A61 (2005), p. c147.
[2] I. Dix et al. ‘The EU BIOXHIT standard test crystal – verfiying Se-MAD beamlines’. In: *Acta Crystallogr* A62 (2006), s21.
[3] T. Gruene et al. ‘Refinement of Macromolecular Structures against Neutron Data with SHELXL-2013’. In: *J. Appl. Crystallogr.* 47 (2014), pp. 462–466.